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Query Match      35.3%;   Score 613;   DB 8;   Length 2072;
Best Local Similarity 63.2%;   Pred. No. 8.6e-160;
Matches 1008;   Conservative 0;   Mismatches 555;   Indels 32;   Gaps 3;

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QY 47 CCGAAAGAAAGATGGCGGCTGAACATAACCCTCAGATGGCGGAGTCGCTATTGGAAA 106
Db 265 CCGCGCGGCACAATCTCGCAAAAGCTCACCCCGCATGGCGGAATCGCTACTCGAGC 324

QY 107 ACAACCCGCTCTCAGGAACGAGACGGCCGGCATGGACAAGACAAGGCCGGCGGAGGCAA 166
Db 325 TGAACCCGGCCCTACGAAGCGAGCTTGCTGGAATGGATAAGGAAAAGGCACAGAAGCTC 384

QY 167 TGCGCAAAATGAACATTGCCGAATTGCTGACAGGCTTGTGAGTTTCCGGGAAGAACCGA 226

385 TTCCGACATGACATTTTGGATCTCCACCGGCTTATCTGTAACCGGAAGAACAA 444
 QY 227 AGAATATGGCTTGTACAAAGTTTGGCAACGACGCTGTGCCCGGATTCATGAGAGA 286
 DB 445 AGAATATGGCTTGTACAAAGTTTGGCAACGACGCTGTGCCCGGATTCATGAGAGA 286
 QY 287 GTACCGATA---CTGGGGGCGCTTAAAGATCATGATCCCTGAAAGAGCTCAAGAAC 343
 DB 505 AGACCGAGAGCCCTGACGCGCGGATCAAAATGATGAACTTGAACCAAGGCTTCTCGGAGC 564
 QY 344 CGAATGCGCTGCTTGAAGATTTGAAGGCGGACCTGACCTGACCAAGAGATGAGC 403
 DB 565 CTATTCGCTGATGATGACGATTCGAGGCTTACCTGATGATGATGATGAGGCGAGC 624
 QY 404 TGCAGAGCTGTGGGATTTGTGACGATTCATGATGATGATGATGATGATGATGATG 463
 DB 625 TGAAGAGATTTTATGATTTCTGCGGACCATTCATGATGATGATGATGATGATGATG 684
 QY 464 GATTCAGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 523
 DB 685 GATTCAGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 725
 QY 524 TTTCACCGGCTTGGGAGGCTTGTGATTTTGAAGCGCTGACATTTTGAACGATGAGC 583
 DB 726 TTCTGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 785
 QY 584 TCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 643
 DB 786 ACTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 845
 QY 644 CAATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703
 DB 846 AAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 905
 QY 704 CAAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763
 DB 906 AAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 965
 QY 764 CCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 823
 DB 966 GCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1025
 QY 824 CTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 883
 DB 1026 ATATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085
 QY 884 TTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 943
 DB 1086 GTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1145
 QY 944 GCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1003
 DB 1146 GTCCCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1205
 QY 1004 CAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1063
 DB 1206 AATGCAAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1265
 QY 1064 TGCCTGCAACGAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1123
 DB 1266 TGACCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1325
 QY 1124 GAGGCTGCAAG 1183
 DB 1326 ACCCGAG 1385
 QY 1184 CACGAGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1243
 DB 1386 TACGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1445
 QY 1244 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1303
 DB 1446 GAAGCTTAAAGCGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1505

QY 1304 GAAGCTCTCAAG 1363
 DB 1506 AAGAGGCTTAAAG 1565
 QY 1364 GGTACATGAG 1413
 DB 1566 GTTACGCTTAAAG 1625
 QY 1414 GACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1473
 DB 1626 CCAAGCGGCTTCCAG 1685
 QY 1474 TGTCTGCTGCAAG 1533
 DB 1686 GCTTCTGCTGCAAG 1745
 QY 1534 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1593
 DB 1746 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1805
 QY 1594 AAG 1628
 DB 1806 GAAG 1840

RESULT 6
 SPC2G2 36493 bp DNA linear PLN 23-MAY-1999
 S.pombe chromosome II cosmid c262.
 AL022103.1 GI:2956767
 60S ribosomal protein l16-c; beta transducin; beta-adaptin; cell
 division protein ftsj homolog; deoxyribidylate deaminase;
 glycylpeptide n-tetradecanoyl transferase; histidyl-tryptophan
 synthetase; mannose-6-phosphate isomerase; phosphatidylinositol
 family protein; tetrahydrofolate synthase; rpl16c; sum
 transporter; WD repeat protein; WD-40 repeat.
 Schizosaccharomyces pombe.
 Schizosaccharomyces pombe.
 Eukaryota; Nungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.
 1 (bases 1 to 36493)
 Wood, V., Rajandream, A.A., Barrell, B.G., Devlin, K. and Churcher, C.M.
 Direct Submission
 Submitted (04-MAR-1998) European Schizosaccharomycetes genome
 sequencing project, Sanger Centre, The Wellcome Trust Genome
 Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

Notes:
 Details of yeast sequencing at the Sanger Centre are available on
 the World Wide Web.
 (URL: <http://www.sanger.ac.uk/projects/S.pombe/>)
 During 1995 to 1996 about 80% of S. pombe chromosome I was
 sequenced by the Sanger Centre. The sequencing of the S. pombe
 genome is now being continued with funding from the European
 Commission. Fourteen European sequencing laboratories, including
 the Sanger Centre, are participating in the project.
 Protein coding regions (CDS) have been predicted with the help of
 computer analysis using the gene-finder program in Pombase (an ACDB
 supplied by the program Sp3splice. CAUTION: It is possible that for
 any individual CDS we may have underestimated or overestimated the
 number of introns/exons or we may not have chosen the correct
 splice donor/acceptor sites.
 CDS are numbered using the following system eg SPC25H2.01c. SP (S.
 pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS), c
 (complementary strand).
 The more significant matches with motifs in the PROSITE database
 are also included but some of these may be fortuitous.
 The length in codons is given for each CDS.
 IMPORTANT: This sequence MAY NOT be the entire insert of the